Stephanie M Gogarten

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5856622/publications.pdf

Version: 2024-02-01

64 papers 9,090 citations

36 h-index 63 g-index

75 all docs

75 docs citations

75 times ranked 19049 citing authors

#	Article	IF	CITATIONS
1	A high-performance computing toolset for relatedness and principal component analysis of SNP data. Bioinformatics, 2012, 28, 3326-3328.	4.1	1,939
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
3	Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics, 2012, 44, 642-650.	21.4	511
4	THE ACS NEARBY GALAXY SURVEY TREASURY. Astrophysical Journal, Supplement Series, 2009, 183, 67-108.	7.7	435
5	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
6	THE ACS NEARBY GALAXY SURVEY TREASURY. VIII. THE GLOBAL STAR FORMATION HISTORIES OF 60 DWARF GALAXIES IN THE LOCAL VOLUME. Astrophysical Journal, 2011, 739, 5.	4.5	295
7	<tt>VariantAnnotation</tt> : a <tt>Bioconductor</tt> package for exploration and annotation of genetic variants. Bioinformatics, 2014, 30, 2076-2078.	4.1	293
8	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	1.3	292
9	THE PANCHROMATIC HUBBLE ANDROMEDA TREASURY. Astrophysical Journal, Supplement Series, 2012, 200, 18.	7.7	269
10	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2016, 98, 165-184.	6.2	266
11	Genetic association testing using the GENESIS R/Bioconductor package. Bioinformatics, 2019, 35, 5346-5348.	4.1	260
12	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. Bioinformatics, 2012, 28, 3329-3331.	4.1	177
13	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma in Caucasians from the USA. Human Molecular Genetics, 2011, 20, 4707-4713.	2.9	156
14	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
15	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
16	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. JAMA - Journal of the American Medical Association, 2018, 320, 2354.	7.4	144
17	Interplay of Genetic Risk Factors (<i>CHRNA5</i> - <i>CHRNA3</i> - <i>CHRNB4</i>) and Cessation Treatments in Smoking Cessation Success. American Journal of Psychiatry, 2012, 169, 735-742.	7.2	138
18	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138

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19	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
20	SeqArrayâ€"a storage-efficient high-performance data format for WGS variant calls. Bioinformatics, 2017, 33, 2251-2257.	4.1	127
21	Association of clonal hematopoiesis with chronic obstructive pulmonary disease. Blood, 2022, 139, 357-368.	1.4	106
22	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
23	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. Depression and Anxiety, 2016, 33, 265-280.	4.1	99
24	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
25	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
26	THE ADVANCED CAMERA FOR SURVEYS NEARBY GALAXY SURVEY TREASURY. V. RADIAL STAR FORMATION HISTORY OF NGC 300. Astrophysical Journal, 2010, 712, 858-874.	4.5	86
27	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
28	Genome-Wide Meta-Analysis of Homocysteine and Methionine Metabolism Identifies Five One Carbon Metabolism Loci and a Novel Association of ALDH1L1 with Ischemic Stroke. PLoS Genetics, 2014, 10, e1004214.	3.5	69
29	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
30	A fully adjusted twoâ€stage procedure for rankâ€normalization in genetic association studies. Genetic Epidemiology, 2019, 43, 263-275.	1.3	60
31	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
32	THE ACS NEARBY GALAXY SURVEY TREASURY. I. THE STAR FORMATION HISTORY OF THE M81 OUTER DISK. Astronomical Journal, 2009, 137, 419-430.	4.7	57
33	Local Ancestry Inference in a Large US-Based Hispanic/Latino Study: Hispanic Community Health Study/Study of Latinos (HCHS/SOL). G3: Genes, Genomes, Genetics, 2016, 6, 1525-1534.	1.8	51
34	THE NGC 300 TRANSIENT: AN ALTERNATIVE METHOD FOR MEASURING PROGENITOR MASSES. Astrophysical Journal, 2009, 703, 300-310.	4.5	50
35	HOW TYPICAL ARE THE LOCAL GROUP DWARF GALAXIES?. Astrophysical Journal, 2011, 743, 8.	4.5	49
36	THE ACS NEARBY GALAXY SURVEY TREASURY. II. YOUNG STARS AND THEIR RELATION TO $H\hat{I}\pm$ AND UV EMISSION TIMESCALES IN THE M81 OUTER DISK. Astrophysical Journal, 2009, 691, 115-130.	4.5	45

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37	Genomeâ€wide association study of generalized anxiety symptoms in the Hispanic Community Health Study/Study of Latinos. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 132-143.	1.7	37
38	Multi-Omics Analysis Reveals a HIF Network and Hub Gene EPAS1 Associated with Lung Adenocarcinoma. EBioMedicine, 2018, 32, 93-101.	6.1	35
39	Shared genetic susceptibility of vascular-related biomarkers with ischemic and recurrent stroke. Neurology, 2016, 86, 351-359.	1.1	33
40	THE ADVANCED CAMERA FOR SURVEYS NEARBY GALAXY SURVEY TREASURY. IV. THE STAR FORMATION HISTORY OF NGC 2976. Astrophysical Journal, 2010, 709, 135-148.	4.5	32
41	The Ultraviolet, Optical, and Infrared Properties of Sloan Digital Sky Survey Sources Detected byGALEX. Astronomical Journal, 2005, 130, 1022-1036.	4.7	31
42	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
43	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
44	<i>SPITZER</i> OBSERVATIONS OF A GRAVITATIONALLY LENSED QUASAR, QSO 2237+0305. Astrophysical Journal, 2009, 697, 1010-1019.	4.5	27
45	Genetic Associations with Plasma B12, B6, and Folate Levels in an Ischemic Stroke Population from the Vitamin Intervention for Stroke Prevention (VISP) Trial. Frontiers in Public Health, 2014, 2, 112.	2.7	23
46	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	3.3	23
47	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Nicotine and Tobacco Research, 2018, 20, 448-457.	2.6	21
48	THE HISTORY OF STAR FORMATION IN GALAXY DISKS IN THE LOCAL VOLUME AS MEASURED BY THE ADVANCED CAMERA FOR SURVEYS NEARBY GALAXY SURVEY TREASURY. Astrophysical Journal Letters, 2011, 734, L22.	8.3	18
49	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.7	18
50	Identification of putative causal loci in whole-genome sequencing data via knockoff statistics. Nature Communications, 2021, 12, 3152.	12.8	17
51	Metaâ€Analysis of Genomeâ€Wide Association Studies with Correlated Individuals: Application to the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Genetic Epidemiology, 2016, 40, 492-501.	1.3	16
52	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16
53	Genome-wide association study of depressive symptoms in the Hispanic Community Health Study/Study of Latinos. Journal of Psychiatric Research, 2018, 99, 167-176.	3.1	15
54	Genome-wide association study of PR interval in Hispanics/Latinos identifies novel locus at <i>ID2</i> Heart, 2018, 104, 904-911.	2.9	12

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55	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. Journal of Medical Genetics, 2017, 54, 313-323.	3.2	9
56	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL. Human Molecular Genetics, 2021, 30, 2190-2204.	2.9	8
57	Genetic variation near <scp><i>IRS</i></scp> <i>1</i> <is <scp="" a="" adiposity="" and="" associated="" favorable="" in="" metabolic="" profile="" with="">U.<scp>S.</scp><scp>H</scp>ispanics/<scp>L</scp>atinos. Obesity, 2016, 24, 2407-2413.</is>	3.0	5
58	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. Scientific Reports, 2018, 8, 5675.	3.3	4
59	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. PLoS ONE, 2021, 16, e0253611.	2.5	4
60	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traitsâ€"The Hispanic/Latino Anthropometry Consortium. Human Genetics and Genomics Advances, 2022, 3, 100099.	1.7	3
61	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. Human Genetics and Genomics Advances, 2021, 2, 100040.	1.7	2
62	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. Nature Communications, 2021, 12, 3506.	12.8	1
63	Accounting for population structure in genetic studies of cystic fibrosis. Human Genetics and Genomics Advances, 2022, 3, 100117.	1.7	1
64	The Size-Luminosity Relation of Disk Galaxies in EDisCS Clusters. Proceedings of the International Astronomical Union, 2006, 2, 201-201.	0.0	0